

SEQUENCE LISTING

<110> Gao, Zeren

<120> MURINE CYTOKINE RECEPTOR

<130> 00-46C1

<150> US 09/899,471

<151> 2001-07-05

<150> US 60/216,446

<151> 2000-07-06

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2256

<212> DNA

<213> Mus musculus

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<221> CDS

<222> (197)...(2218)

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caggggcgag ggggtctgcc ccccttgggg gggcaggacg gggcctcagg cctgggtgct 180
gtccggcacc tggaag atg cct gtg tcc tgg ttc ctg ctg tcc ttg gca ctg 232
Met Pro Val Ser Trp Phe Leu Leu Ser Leu Ala Leu
1 5 10
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Gly Arg Asn Pro Val Val Val Ser Leu Glu Arg Leu Met Glu Pro Gln
15 20 25
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Asp Val Leu Cys Leu Pro Gly Ser Leu Gln Ser Ala Pro Gly Pro Val
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Leu Val Pro Thr Arg Leu Gln Thr Glu Leu Val Leu Arg Cys Pro Gln
65 70 75
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aag aca gat tgc gcc ctc cgt gtc cgt gtg gtg gtc cac ttg gcc gtg 472
Lys Thr Asp Cys Ala Leu Arg Val Arg Val Val Val His Leu Ala Val
80 85 90
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His Gly His Trp Ala Glu Pro Glu Glu Ala Gly Lys Ser Asp Ser Glu
95 100 105
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Leu Gln Glu Ser Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
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Val Cys Ala Leu Glu Pro Ser Gly Cys Thr Pro Leu Pro Ser Met Ala	
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Ser Thr Arg Ala Ala Arg Leu Gly Glu Glu Leu Leu Gln Asp Phe Arg	
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Trp Ala Cys Pro Met Asp Lys Tyr Ile His Arg Arg Trp Val Leu Val	
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His Gln Arg Arg Arg Ile Leu Gln Glu Gly Gly Val Val Ile Leu Leu	
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Thr Val Glu Pro Gly Pro His Asp Ala Leu Ala Ala Trp Leu Ser Cys	
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Val Leu Pro Asp Phe Leu Gln Gly Arg Ala Thr Gly Arg Tyr Val Gly	
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Val Tyr Phe Asp Gly Leu Leu His Pro Asp Ser Val Pro Ser Pro Phe	
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Thr Ser Ser Ser Glu Ala Pro Gly Cys Cys Glu Glu Trp Asp Leu Gly	655	660	665	
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325                330                335
Pro Asn Leu Cys Val Gln Val Ser Thr Trp Glu Lys Val Gln Leu Gln
340                345                350
Ala Cys Ser Trp Ala Asp Ser Leu Gly Pro Phe Lys Asp Asp Met Leu
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370                375                380
Glu Pro Ser Gly Cys Thr Pro Leu Pro Ser Met Ala Ser Thr Arg Ala
385                390                395                400
Ala Arg Leu Gly Glu Glu Leu Leu Gln Asp Phe Arg Ser His Gln Cys
405                410                415
Met Gln Leu Trp Asn Asp Asp Asn Met Gly Ser Leu Trp Ala Cys Pro
420                425                430
Met Asp Lys Tyr Ile His Arg Arg Trp Val Leu Val Trp Leu Ala Cys
435                440                445
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450                455                460
Arg Arg Lys Ala Ala Arg Gly Ser Arg Thr Ala Leu Leu Leu His Ser
465                470                475                480
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485                490                495
Leu Ser Gln Met Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg
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Glu Leu Ser Ala His Gly Ala Leu Ala Trp Phe His His Gln Arg Arg
515                520                525
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Ala Val Ala Gln Cys Gln Gln Trp Leu Gln Leu Gln Thr Val Glu Pro
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Gly Pro His Asp Ala Leu Ala Ala Trp Leu Ser Cys Val Leu Pro Asp
565                570                575
Phe Leu Gln Gly Arg Ala Thr Gly Arg Tyr Val Gly Val Tyr Phe Asp
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Gly Leu Leu His Pro Asp Ser Val Pro Ser Pro Phe Arg Val Ala Pro
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Leu Phe Ser Leu Pro Thr Gln Leu Pro Ala Phe Leu Asp Ala Leu Gln
610                615                620
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625                630                635                640
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<210> 3

<211> 2022

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate sequence encoding the polypeptide of
SEQ ID NO:2.

<221> variation

<222> (1)...(2022)

<223> n = A, T, G or C

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gcnytnmgng	tnmgngtngt	ngtncaaytn	gcngtncaayg	gncaytgggc	ngarccngar	300
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<220>

<221> CDS

<222> (197)...(2290)

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15 20 25	

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Lys	Thr	Gly	Leu	Asn	Asn	Thr	Ser	Val	Cys	Ala	Leu	Glu	Pro	Ser	Gly	
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Cys	Thr	Pro	Leu	Pro	Ser	Met	Ala	Ser	Thr	Arg	Ala	Ala	Arg	Leu	Gly	
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Glu	Glu	Leu	Leu	Gln	Asp	Phe	Arg	Ser	His	Gln	Cys	Met	Gln	Leu	Trp	
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Asn	Asp	Asp	Asn	Met	Gly	Ser	Leu	Trp	Ala	Cys	Pro	Met	Asp	Lys	Tyr	
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Ile	His	Arg	Arg	Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	Ala	
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gcg	gcg	ctt	ttc	ttc	ttc	ctc	ctt	cta	aaa	aag	gac	cgc	agg	aaa	gcg	1672
Ala	Ala	Leu	Phe	Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys	Ala	
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Ala	Arg	Gly	Ser	Arg	Thr	Ala	Leu	Leu	Leu	His	Ser	Ala	Asp	Gly	Ala	
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Gly	Tyr	Glu	Arg	Leu	Val	Gly	Ala	Leu	Ala	Ser	Ala	Leu	Ser	Gln	Met	
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Pro	Leu	Arg	Val	Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	

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His Gly Ala Leu Ala Trp Phe His His Gln Arg Arg Arg Ile Leu Gln				
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Pro Asp Ser Val Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser Leu				
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<211> 698

<212> PRT

<213> Mus musculus

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Cys	Ser	Leu	Gly	Leu	Ser	Cys	His	Leu	Trp	Asp	Gly	Asp	Val	Leu	Cys
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Ala	Leu	Arg	Val	Arg	Val	Val	Val	His	Leu	Ala	Val	His	Gly	His	Trp
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Arg	Asn	Ala	Ser	Leu	Gln	Ala	Gln	Val	Val	Leu	Ser	Phe	Gln	Ala	Tyr
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Val	Gln	Pro	Gly	Gln	Ser	Val	Gly	Ser	Ala	Val	Phe	Asp	Cys	Phe	Glu
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Ala	Ser	Leu	Gly	Ala	Glu	Val	Gln	Ile	Trp	Ser	Tyr	Thr	Lys	Pro	Arg
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Tyr	Gln	Lys	Glu	Leu	Asn	Leu	Thr	Gln	Gln	Leu	Pro	Asp	Cys	Arg	Gly
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Leu	Glu	Val	Arg	Asp	Ser	Ile	Gln	Ser	Cys	Trp	Val	Leu	Pro	Trp	Leu
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Trp	Val	Leu	Val	Trp	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Ala	Ala	Leu	Phe
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Phe	Phe	Leu	Leu	Leu	Lys	Lys	Asp	Arg	Arg	Lys	Ala	Ala	Arg	Gly	Ser
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Arg	Thr	Ala	Leu	Leu	His	Ser	Ala	Asp	Gly	Ala	Gly	Tyr	Glu	Arg	
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Ala	Val	Asp	Leu	Trp	Ser	Arg	Arg	Glu	Leu	Ser	Ala	His	Gly	Ala	Leu
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Ala	Trp	Phe	His	His	Gln	Arg	Arg	Arg	Ile	Leu	Gln	Glu	Gly	Gly	Val
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Val	Ile	Leu	Leu	Phe	Ser	Pro	Ala	Ala	Val	Ala	Gln	Cys	Gln	Gln	Trp
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Leu	Gln	Leu	Gln	Thr	Val	Glu	Pro	Gly	Pro	His	Asp	Ala	Leu	Ala	Ala
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      610                      615                      620
Pro Ser Pro Phe Arg Val Ala Pro Leu Phe Ser Leu Pro Thr Gln Leu
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Arg Pro Ala Asp Arg Val Glu Arg Val Thr Gln Ala Leu Arg Ser Ala
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<211> 2094

<212> DNA

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<220>

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SEQ ID NO:5.

<221> variation

<222> (1)...(2094)

<223> n = A, T, G or C

<400> 6

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<220>
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<210> 8
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 35 40 45
 Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val Leu Ala Pro Thr
 50 55 60
 His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln Lys Glu Thr Asp Cys
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 Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
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 Glu Glu Pro Glu Asp Glu Glu Lys Phe Gly Gly Ala Ala Asp Ser Gly
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 Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
 115 120 125
 Phe Gln Ala Tyr Pro Thr Ala Arg Cys Val Leu Leu Glu Val Gln Val
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 Pro Ala Ala Leu Val Gln Phe Gly Gln Ser Val Gly Ser Val Val Tyr
 145 150 155 160
 Asp Cys Phe Glu Ala Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr
 165 170 175
 Thr Gln Pro Arg Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro
 180 185 190
 Ala Leu Pro Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu
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 Asn Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr
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 Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu
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 Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr Asn Ile
 260 265 270
 Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala
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 Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp Arg Ala Pro Gly Gly

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Cys	Val	Gln	Val	Asn	Ser	Ser	Glu	Lys	Leu	Gln	Leu	Gln	Glu	Cys	Leu
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Trp	Ala	Asp	Ser	Leu	Gly	Pro	Leu	Lys	Asp	Asp	Val	Leu	Leu	Leu	Glu
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Ser	Arg	Ala	Leu	Gln	Pro	Ala	Leu	Asp	Ser	Tyr	Phe	His	Pro	Pro	Gly
Thr	Pro	Ala	Pro	Gly	Arg	Gly	Val	Gly	Pro	Gly	Ala	Gly	Pro	Gly	